1600

RAW SEQUENCE LISTING   DATE: 10/25/2001
PATENT APPLICATION: US/09/582,328   TIME: 13:23:48

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Output Set: N:\CRF3\10252001\I582328.raw

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  3 <110> APPLICANT: FORSSMANN, WOLF-GEORG
  4        MAGERT, HANS-JURGEN
  5        STANDKER, LUDGER
  6        KREUZTMANN, PETER
  8 <120> TITLE OF INVENTION: SERINE PROTEINASE INHIBITORS
 10 <130> FILE REFERENCE: 10496/P65678US0
 12 <140> CURRENT APPLICATION NUMBER: 09/582,328
 13 <141> CURRENT FILING DATE: 2000-07-09
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/08424
 16 <151> PRIOR FILING DATE: 1998-12-23
 18 <150> PRIOR APPLICATION NUMBER: DE 197 57 572.2
 19 <151> PRIOR FILING DATE: 1997-12-23
 21 <160> NUMBER OF SEQ ID NOS: 41
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 177
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Unknown Organism
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Unknown Organism: VAKTI-1 amino
 32       acid sequence
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 36  1               5                  10                  15
 38 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
 39                  20                  25                  30
 41 Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
 42              35                  40                  45
 44 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
 45          50                  55                  60
 47 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
 48  65                  70                  75                  80
 50 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
 51                  85                  90                  95
 53 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
 54              100                 105                 110
 56 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
 57              115                 120                 125
 59 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
 60          130                 135                 140
 62 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg
 63 145                 150                 155                 160
 65 Ser Ile Val Ser Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser
 66                  165                 170                 175
 68 Lys
 71 <210> SEQ ID NO: 2
 72 <211> LENGTH: 922
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 74 <213> ORGANISM: Unknown Organism
 76 <220> FEATURE:
 77 <223> OTHER INFORMATION: Description of Unknown Organism: VATKI-2 amino
 78      acid sequence
 80 <400> SEQUENCE: 2
 81 Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
 82   1               5                  10                  15
 84 Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
 85              20                  25                  30
 87 Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
 88          35                  40                  45
 90 Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
 91      50                  55                  60
 93 Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
 94  65                  70                  75                  80
 96 Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
 97              85                  90                  95
 99 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
100              100                 105                 110
102 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
103          115                 120                 125
105 Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
106      130                 135                 140
108 Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
109 145                 150                 155                 160
111 Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr
112              165                 170                 175
114 Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
115              180                 185                 190
117 Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
118          195                 200                 205
120 Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
121      210                 215                 220
123 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
124 225                 230                 235                 240
126 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
127              245                 250                 255
129 Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
130          260                 265                 270
132 Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
133          275                 280                 285
135 Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
136      290                 295                 300
138 Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
139 305                 310                 315                 320
141 Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
142              325                 330                 335
144 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg
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145            340            345            350
147 Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
148         355            360            365
150 Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
151     370            375            380
153 Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
154 385            390            395            400
156 Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Lys Lys Lys
157            405            410            415
159 Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
160            420            425            430
162 Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
163         435            440            445
165 Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
166     450            455            460
168 Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
169 465            470            475            480
171 Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
172            485            490            495
174 Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
175         500            505            510
177 Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
178         515            520            525
180 Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
181     530            535            540
183 Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
184 545            550            555            560
186 Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
187            565            570            575
189 Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
190         580            585            590
192 Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
193         595            600            605
195 Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
196     610            615            620
198 Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
199 625            630            635            640
201 Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
202            645            650            655
204 Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe
205         660            665            670
207 Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg
208         675            680            685
210 Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Asn Thr Gln
211     690            695            700
213 Asp Glu Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser
214 705            710            715            720
216 Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr
217            725            730            735
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219 Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu
220             740             745             750
222 Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu
223         755             760             765
225 Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly
226     770             775             780
228 Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly
229 785             790             795             800
231 Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg
232             805             810             815
234 Glu Ala Ala Glu Lys Lys Arg Lys Arg Met Lys Thr Gly Ala Ile Gln
235             820             825             830
237 Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys
238         835             840             845
240 Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro
241     850             855             860
243 Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile
244 865             870             875             880
246 Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu
247             885             890             895
249 Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln
250         900             905             910
252 Arg Met Ser Ala Val Asn Phe Glu Thr Ile
253         915             920
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 55
258 <212> TYPE: PRT
259 <213> ORGANISM: Unknown Organism
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Unknown Organism: HF 6479 amino
263       acid sequence
265 <400> SEQUENCE: 3
266 Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe Met Lys
267 1               5               10              15
269 Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln Ser Leu
270             20              25              30
272 Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met Ile Leu
273         35              40              45
275 Glu Lys Glu Ala Lys Ser Gln
276     50              55
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 68
281 <212> TYPE: PRT
282 <213> ORGANISM: Unknown Organism
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Unknown Organism: HF 7665 amino
286       acid sequence
288 <400> SEQUENCE: 4
289 Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg
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290    1                 5                   10                  15
292 Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro
293             20                  25                  30
295 Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys
296         35                  40                  45
298 Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys Lys Glu Gly
299         50                  55                  60
301 Glu Ser Arg Asn
302  65
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 748
307 <212> TYPE: DNA
308 <213> ORGANISM: Unknown Organism
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Unknown Organism: VAKTI-1 cDNA
312        sequence
314 <220> FEATURE:
315 <221> NAME/KEY: CDS
316 <222> LOCATION: (43)..(573)
318 <400> SEQUENCE: 5
319 atgcatggag tggacctgta ggcgacttgc atcgtcttca ac atg aag ata gcc      54
320                                                 Met Lys Ile Ala
321                                                  1
323 aca gtg tca gtg ctt ctg ccc ttg gct ctt tgc ctc ata caa gat gct    102
324 Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala
325   5                 10                  15                  20
327 gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt    150
328 Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe
329              25                  30                  35
331 atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa    198
332 Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln
333          40                  45                  50
335 agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg    246
336 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met
337          55                  60                  65
339 ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca    294
340 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala
341      70                  75                  80
343 aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt    342
344 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe
345   85                  90                  95                 100
347 aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa    390
348 Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu
349              105                 110                 115
351 gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg    438
352 Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu
353              120                 125                 130
355 tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa    486
356 Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu
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VERIFICATION SUMMARY
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